

*In the Claims:*

Please amend the claims as follows:

C1 33. (Thrice amended) A method for detecting a ligand within a test sample, comprising contacting a test sample with a polypeptide comprising a segment selected from the group consisting of:

(a) amino acid residues 141 to 337 of SEQ ID NO:2; and

(b) [an allelic variant of (a),] an amino acid sequence that is at least 90% identical to amino acid residues 141 to 337 of SEQ ID NO:2,

and detecting binding of said polypeptide to ligand in the sample.

C2 34. (Amended) A method according to claim 33 wherein said polypeptide comprises either amino acid residues 25 to 337 of SEQ ID NO:2 [or an allelic variant of SEQ ID NO:2] or amino acid residues 25 to 337 of SEQ ID NO:4.

**REMARKS**

Although claims 1-39 are pending in the present application, claims 1-32 and 39 have been withdrawn from consideration. Applicants have amended the claims to clarify certain aspects of their invention. Support for the language "an amino acid sequence that is at least 90% identical to amino acid residues 141 to 337 of SEQ ID NO:2," in amended claim 33 can be found at least on page 13, lines 22-25, of the application. Additional support can be found in the disclosure of amino acid sequences of a second human clone (SEQ ID NO:4) and a macaque clone (SEQ ID NO:7) that are 99% and 92% identical, respectively, to amino acid residues 141 to 337 of SEQ ID NO:2 (see page 35 (lines 22-24), and page 39 (lines 8-12)). Support for the language "residues 25 to 337 of SEQ ID NO:4," in amended claim 34 can be found at least on page 28, lines 17-19. For the Examiner's convenience, applicants have attached a copy of the amended claims to this response. No new matter has been added by way of these amendments.

As a preliminary matter, applicants thank the Examiner for the telephone interview conducted on January 21, 1999, with applicants' representative. During the discussion, the Examiner requested applicants to clearly delineate support for the claim language relating to percent identity. As noted in the previous paragraph, the specification supports the recitation of "at least 90% identical" to amino acid residues 141-337 of SEQ ID NO:2, and the specification provides two examples of sequences that share this level of identity. In addition, the specification discloses that amino acid